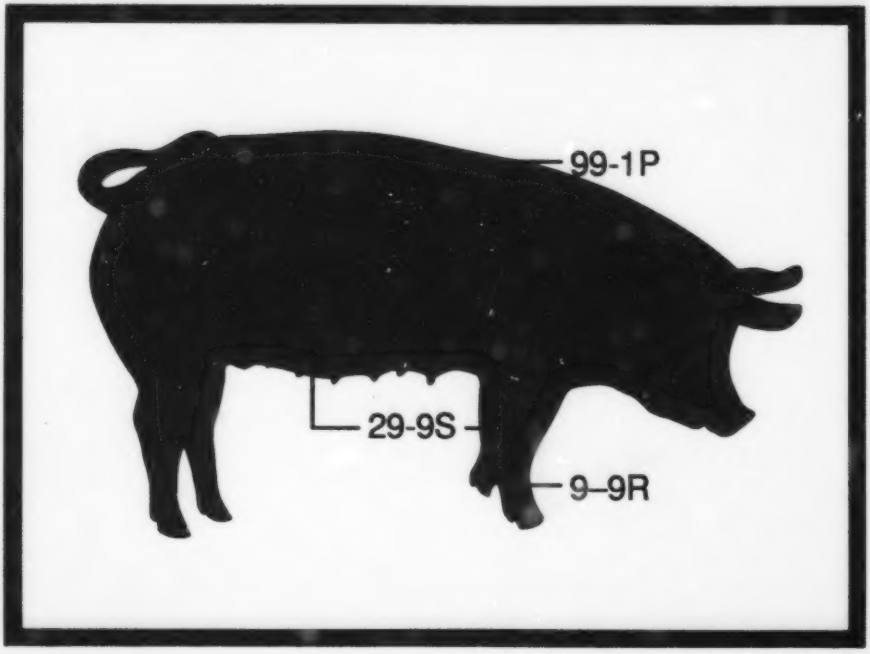
Agriculture Canada

Publication 1877/E

Practical guide to swine breeding



Canada

Printed with the financial support of the following:
Swine Section, Animal Industry Branch, Nova Scotia Department of Agriculture and Marketing

Practical guide to swine breeding

Robert M. McKay
Research Station
Brandon, Manitoba

Agriculture Canada Publication 1877/E
available from
Communications Branch, Agriculture Canada
Ottawa, Ont. K1A 0C7

©Minister of Supply and Services Canada 1992
Cat. No. A63-1877/1992E ISBN 0-662-19241-9
Printed 1992 3.2M-06:92

Produced by Research Program Service

Également disponible en français sous le titre
Guide de l'amélioration génétique des porcins

93-00237/

Contents

Preface 5
Acknowledgments 6

Breed distribution in Canada 7

Genetic improvement 8
Performance testing 9
Artificial insemination 10
Record keeping 10

Selection methods 14
Tandem selection 14
Independent culling levels 15
Selection index 16
EBV selection index 21
Sow productivity and management program 22

Crossbreeding 22
Terminal crossbreeding 25
  Single cross 25
  Backcross 25
  Three-breed cross 26
  Four-breed cross 26
Rotational crossbreeding 27
  Two-breed or crisscross rotation 27
  Three-breed rotation 28
Genetic lag 30

Genetic defects and abnormalities 32
Recessive genes 32
Dominant genes 35
Halothane gene 37
Defects and the breeding herd 38

Inbreeding 38
Calculation of inbreeding coefficients 39
Practical management of inbreeding 46

Where do we go from here? 47

Glossary of terms 49

Preface

In 1962, Dr. Howard Fredeen of the Research Station at Lacombe, Alta., wrote a technical bulletin on swine breeding (Agric. Can. Publ. 1127), which was the only one of its kind that has been produced by Agriculture Canada. Since then significant changes have occurred in swine breeding. These changes include the establishment of the Record of Performance program for swine, the advent of a carcass grading system that has a direct relationship with swine improvement, and the emergence of breeding companies. This new publication will serve as an extension of Dr. Fredeen's bulletin, because most of the principles outlined in his publication remain valid today.

Acknowledgments

The author gratefully acknowledges the contribution of Mrs. Sharon Ramsay, Information Officer; Mrs. Carol Enns, Librarian; and Dr. Gunther Rahnefeld, Beef Cattle Geneticist and Animal Science Section Head, Agriculture Canada Research Station, Brandon, Man.; Mr. Gerry Bruins, Livestock Division, Agriculture Canada, Ottawa, Ont.; Mr. Ron Black, Canadian National Livestock Records in Ottawa, Ont.; Mr. George Croome, Lacombe Breeders Association; Dr. Robert J. Parker, Department of Animal Science, University of Manitoba, Winnipeg, Man.; and Mr. Clarence Froese, Sales Manager—Hog Division, Pur-A-Tone, Niverville, Man.

The following deserve special appreciation for constructively reviewing this bulletin: Dr. Howard Fredeen, Geneticist, formerly of the Agriculture Canada Research Station, Lacombe, Alta.; Dr. Robert Parker, Professor of Animal Science, University of Manitoba, Winnipeg, Man.; Dr. Rodger Johnson, Professor of Animal Science, University of Nebraska, Lincoln, Nebr.; Dr. Bruce Allen, Geneticist, Pig Improvement Canada, Acme, Alta.; and Mr. Clarence Froese, Sales Manager—Hog Division, Pur-A-Tone, Niverville, Man.

Breed distribution in Canada

The predominant breeds in the Canadian swine industry were determined from registration and performance-testing records. Table 1 summarizes the breed distribution. Excluding the effects of commercial boars and gilts (crossbred or unregistered purebred pigs), the Yorkshire and Landrace breeds dominate Canadian swine. The Duroc, Hampshire, and Lacombe breeds comprise the second tier, with the remaining breeds occupying the lowest tier. Including the commercial boars only slightly alters the picture, because they become part of the second tier.

It is in the home-tested gilts where the full effect of the commercial pig is felt. The commercial gilts not only belong to the first tier but dominate it. The dominance of the commercial gilt, compared with the Yorkshire and Landrace breeds, is more dramatic than shown by this table. From 1982 to 1988, the commercial pigs represented more than 40% of the home-tested gilts and, from 1986 to 1988, that percentage exceeded 46%.

The increased use of crossbred gilts and boars that has occurred throughout the 1980s has resulted in part from the efforts of private breeding companies. These companies, through their large herd sizes and selection programs, can provide sources of high-quality breeding stock in terms of genetic quality and structural soundness.

Table 1 Registrations (1970, 1974, 1977, 1980, 1983, 1986, and 1989) and station-tested boars and home-tested boars and gilts (1973 to 1988) by breed

Breed	Registrations	Station-tested boars	Home-tested	
			Boars	Gilts
		%		
Yorkshire	46.06	46.44	36.27	29.03
Landrace	28.63	29.87	26.17	20.31
Duroc	10.09	10.06	10.90	4.70
Hampshire	8.27	5.31	7.24	2.94
Lacombe	5.14	4.70	4.58	2.36
Other*	1.81	0.72	1.83	1.12
Commercial	–	2.91	13.01	39.54
Number of pigs	162 319	52 988	422 116	977 001

* Berkshire, Chester White, Tamworth, Poland China, Welsh, Large Black, Saddleback (British and Wessex), Spot, Pietrain, Managra, Red Wattles, and Newfoundland.

Genetic improvement

Genetic improvement is the increase in frequency or number of desirable genes within a herd or population that results in enhanced performance. In swine, genetic improvement is guided by the breeder through the selection that is practiced. Selection, however, is not the only means of changing gene frequency. Other ways are migration, mutation, and random drift.

Selection

Selection is the practice of allowing some pigs to produce more offspring than others. There are two forms of selection active within any herd: natural and artificial. Under natural selection, survival is emphasized, whereas artificial selection emphasizes the traits chosen by the breeder.

Migration

Migration, in the context of swine breeding, is both the inflow of genes that occurs when breeding stock is introduced into the herd and the loss of genes when pigs are culled from the herd. Breeding stock can be purchased boars and gilts or simply semen that is purchased from an artificial insemination (AI) stud.

Mutation

Mutation is a change in a gene that produces an alternate form or allele. Unlike selection and migration, which can cause major changes in gene frequency depending upon selection pressure and how much breeding stock is added or culled, mutations cause very slight changes in gene frequency and cannot be controlled by the breeder.

Random drift

Gene frequencies can vary purely by chance, a phenomenon called random drift or chance. The best way to describe random drift is by example. Assume that the frequency of the dominant and recessive genes at some location on a chromosome was 0.6 and 0.4, respectively, in the Yorkshire breed as a whole. If a breeder purchased a herd of Yorkshires from breeder A, the frequency of the dominant gene could be 0.3 and the recessive gene 0.7 in the purchased herd. The difference in gene frequency between this purchased herd and the Yorkshire breed is due to chance.

Of the four ways of changing gene frequency, only two—selection and migration—have direct application for the swine breeder.

Performance testing

Record of Performance

Testing of swine began in Canada in 1928 with the Advanced Registry Policy for purebred swine. This policy was expanded in 1934 when a national testing program for purebred swine was formed, based on the Danish progeny test system. In 1935, the Canada Department of Agriculture began to construct test stations across Canada for the purpose of testing purebred swine under similar management and conditions. However, by 1980, H.T. Fredeen had observed that geographical distribution of swine breeders, small herd sizes (usually less than eight sows per herd), and short herd life-spans (less than 5 years), coupled with the inherent difficulties of progeny testing, limited the benefits derived from this system. Starting in 1966, the progeny-testing program was gradually phased out and was replaced by a performance-testing program for boars, which was in place in 1971. The concept of central (station) testing was continued in the era of performance testing. A major increase in performance testing resulted from

- the home-test program, which not only allowed for additional boars to be tested but also for gilts to be evaluated
- the entry of crossbred boars into the test stations and the inclusion of crossbred boars and gilts in the home-test program.

The following traits are evaluated in the station test:

- adjusted backfat to 100 kg liveweight
- adjusted days to 100 kg liveweight
- average daily gain on test (from 30 to 100 kg liveweight)
- feed consumed per kilogram live gain.

In the home test, adjusted backfat and days to 100 kg liveweight are always evaluated, but average daily gain on test is also included if the pigs were weighed when the test period began.

To assess the performance of station- or home-tested pigs, selection indexes were developed. Selection indexes allow the breeder to select for more than one trait at the same time by calculating a value that weights the performance of each trait considered.

The station-test index, initially comprising backfat thickness, average daily gain, and feed conversion, was eventually reduced to include only backfat thickness and average daily gain. The home-test index included backfat thickness and days to 100 kg. In 1985, the selection indexes shifted from using the animal's own performance (phenotype) to using estimated breeding values, an estimate of the genetic merit or the value of an animal as a parent.

A sow productivity program, which is currently being evaluated by Agriculture Canada (Livestock Development Branch), will soon be offered to producers. Its purpose is to assist swine producers in managing and selecting within their breeding herds.

Carcass-grading index

The carcass-grading index, introduced in 1968, was another factor that significantly promoted the use of performance testing. This system, from its inception until 31 March 1986, paid producers based on backfat thickness and hot carcass weight. Since 31 March 1986, in addition to backfat thickness and hot carcass weight, a measure of the loin eye or longissimus dorsi muscle is included in calculating the carcass index.

A definite relationship exists between performance testing and the carcass-grading index. In both systems backfat thickness plays a key role. In terms of carcass settlement, or payment to the producer, backfat thickness receives considerably more weighting than loin eye area. Thus, producers who reduce backfat levels through performance testing will be rewarded with higher carcass indexes.

Artificial insemination

The greatest benefit from using semen from performance-tested boars is the ability to incorporate genes from superior boars at a fraction of the cost of purchasing and caring for live boars. A related benefit is that producers in one region have access to boars standing at stud in other regions. Even if the stud is located in Ontario, for example, and the breeder is in Alberta, fresh semen can be delivered quickly and economically via couriers and the airlines.

From a genetic management standpoint, AI offers an excellent opportunity for the breeder to broaden the genetic base of the herd.

The main difficulty with AI lies in detecting estrus (heat) in the female. Boars can be used to accurately identify estrus, but occasionally the boar will mate with the gilt or sow being checked. An alternative is to use a vasectomized boar. Boars can be vasectomized by the local veterinarian and their semen checked to ensure that they are no longer fertile.

Record keeping

Perhaps the most important aspect in any genetic improvement program is the recording system that is kept and used. Information that is collected on pigs can be divided into litter, postweaning performance, and reproduction records.

Litter records

Litter records should identify all piglets born and provide their teat number, sex, and birth and weaning weights and dates. Other information that will assist producers are vaccination dates and the cause and date of piglet deaths. The unique identification given to piglets usually combines a litter number, an individual number within the litter, and a year letter; it is essential for an effective breeding program. By

knowing the sire and dam of the litter, the breeder can construct the pedigrees for the pig. This knowledge is vital to assess inbreeding and trace genetic defects and abnormalities. Teat number is recorded for use after the pigs have been performance tested. Once the animals have been evaluated on the basis of backfat thickness and growth, the breeder should screen the animals for teat number. This ensures that the breeder does not inadvertently select against teat number. Birth and weaning weights provide a measure of the mothering ability of the sow. They are obtained by summing the gain of each piglet in a litter from birth to weaning and dividing this total by the number of piglets in the litter. When comparing sows based on mothering ability, the number of piglets nursed must be considered. A sow nursing 2 piglets should have greater piglet gains than a sow nursing 12 piglets. These two weights also provide a measure of the growth rate of the piglet. The gain from birth to weaning is divided by the number of days the piglet was nursing the sow. If the breeder does not weigh the piglets at birth, the sow's nursing ability can be approximated by summing the weaning weights of all piglets in the litter. Piglet growth can also be approximated by dividing the weaning weight by the number of days nursed. Calculating either actual or approximate values will provide the necessary information for comparing among piglets or sows, provided that these animals are evaluated by the same means and under similar management and environmental conditions. To illustrate these calculations, consider a litter born at the Agriculture Canada Research Station in Brandon, Man., in 1990, details of which are provided in Table 2.

The main use of individual pig records is for the selecting and culling of exceptional and poor animals, respectively. This information can also be used to pen animals. If the breeder has weaning weights and either actual or approximate measures of growth rate, pigs with similar growth rates can be penned together. If the breeder has insufficient grower–finisher space or if all the boars cannot be grown out, these measures can provide a basis for deciding which boars to keep and which boars to sell or castrate.

Table 2 Litter record for litter 252

Pig number	Sex[b]	Teat number	Weight		Actual		Approx. daily gain (kg)
			Birth (kg)	Weaning[c] (kg)	Gain (kg)	Daily gain (kg)	
252-1Z[a]	B	14	1.0	7.3	6.3	0.18	0.21
252-2Z	B	14	1.1	8.5	7.4	0.21	0.24
252-3Z	B	13	1.1	8.1	7.0	0.20	0.23
252-4Z	B	13	1.3	10.3	9.0	0.26	0.29
252-5Z	G	15	1.2	10.0	8.8	0.25	0.29
252-6Z	G	13	1.2	8.5	7.3	0.21	0.24
252-7Z	G	15	1.3	9.8	8.5	0.24	0.28
252-8Z	G	14	1.1	8.8	7.7	0.22	0.25
252-9Z	G	14	1.3	7.8	6.5	0.19	0.22
252-10Z	G	15	0.9	8.2	7.3	0.21	0.23
Total				87.3	75.8		
Average				8.73	7.58		

[a] 252-1Z refers to the first pig in litter 252 born in 1990 (year letter Z).
[b] B is boar and G is gilt.
[c] Piglets were weaned at 35 days of age.

The measure of mothering ability and the weaned litter size can be used to cull sows. Consider the performance of the six sows in Table 3.

Table 3 Sow performance

Sow	Piglets weaned	Mothering ability	
		Actual	Approx.
13-4Y	5	9.04	10.52
59-8Y	11	6.81	8.18
69-6Y	10	7.58	8.73
78-6Y	9	8.94	10.29
95-6Y	8	6.16	7.28
112-7Y	8	9.46	10.94

From Table 3, it is evident that the rankings would differ depending on whether piglets weaned or mothering ability was considered. For instance, based on weaned litter size, the top three sows are 59-8Y, 69-6Y, and 78-6Y, whereas the top three sows for mothering ability are 112-7Y, 13-4Y, and 78-6Y. A commercial producer would probably cull 13-4Y because the number of weaned pigs is vital for economic survival. A breeder would also cull 13-4Y for the same reason but may decide to cull

95-6Y instead because of the poorer mothering ability. There is no single culling decision that would apply to these six sows. Different breeders or commercial producers would make different culling decisions. Another factor that needs to be considered when comparing sows is the number of litters they have had. Sows that consistently wean large litters with above-average growth should be favored. However, without a written record, the breeder or commercial producer cannot begin to make an informed decision.

Postweaning performance records

Postweaning performance records include probed backfat thickness and days to 100 kg. They are used in calculating the selection index. The concept of selecting pigs based on a selection index is quite simple: the pigs with the largest index value are the best. However, what does a breeder do when two pigs have the same index value and only one is to be kept. Then teat number can come into play. For example, boars A and B both have an index value of 135, but boar A has 12 teats and boar B has 15 teats; select boar B based on it having three more teats than boar A. It goes without saying that in any instance where pigs are selected, they have to be structurally sound and without any visible impediments. If both boars were to have the same index value and teat number then structural differences would be used to select the boar.

Reproduction records

Reproduction records refer to how well the boars and gilts or sows performed during the breeding season. Keep records that include

- percentage of sows successfully bred by the boar
- number of services per conception
- conception rate of the sows at first, second, or third estrus (or heat)
- number of pigs born alive
- number of pigs weaned
- interval between weaning a litter and being rebred
- mothering ability (as previously described)
- condition of the sow
- number of stillbirths, necrotics, and deformed pigs.

How well sows perform in these traits should form the basis for how long they are kept in the breeding herd. Boars that cannot settle sows have little value in the breeding herd or as future sales. Without these records, poor performing boars and sows are kept in herds. If their inferior performance has a genetic basis, then retaining them in the herd permits these genes to spread throughout the herd.

Selection methods

For the swine breeder, selection rarely involves traits that are controlled by a single pair of genes at a specific location on a chromosome. The only exception is selection against some genetic defects. The economically important traits, such as backfat thickness, growth rate, litter size, and carcass merit, are quantitative traits, controlled by many pairs of genes. Each gene pair contributes to the expression of the trait, and with large numbers of gene pairs, there is a wide range in values for the trait. To illustrate how the number of gene pairs can result in a variety of gene pair combinations, consider traits that are controlled by a number of pairs of genes. Assume that each gene pair can have three possible genotypes (i.e., AA, Aa, and aa). For one gene pair, there are three combinations, but for two gene pairs there are three times three or nine combinations. Following this logic, the total possible combinations for the numbers of gene pairs described are

Number of gene pairs	*Total possible combinations*
1	3
2	9
3	27
4	81
5	243
10	59 049
15	14 348 907
20	3 486 784 401
25	847 288 609 443

Faced with these possible combinations of gene pairs and the wide range in values they produce, the breeder has to use different selection techniques to improve the herd.

At least two traits, namely, backfat thickness and growth rate, are of economic importance. To improve more than one trait, the breeder has the choice of using one of three methods:

- tandem selection
- independent culling levels
- selection index.

Tandem selection

Tandem selection is the easiest method to use. The breeder selects for one trait at a time. Once the desired level of performance in the first trait is reached, selection for that trait is stopped and a second trait is selected for. This form of selection is effective if the traits are either favorably related or completely independent. If the traits are unfavorably related, then using this system can be ineffective. Backfat thickness and growth rate are examples of an unfavorable association. If a breeder selected animals

based on backfat alone, there would be a decrease in growth rate. Conversely, if growth rate was the selected trait, backfat levels would increase.

Independent culling levels

Independent culling levels involve setting standards for each of the traits being selected for and selecting only those pigs that meet the standards for each trait. The data in Table 4 are used to show how independent culling levels operate in three easy steps.

Step 1 Set the standards. For backfat thickness, select for less than 14.0 mm. For days to 90 kg, select for less than 170 days.

Step 2 Identify the gilts that meet the standard for backfat thickness (see "Acceptable BF" in Table 4).

Step 3 From the list of gilts that meet the backfat standard, identify those that meet the days to 90 kg standard (see "Acceptable days" in Table 4).

Table 4 Independent culling levels in 33 backfat-probed Hampshire gilts

Gilt	BF[a] (mm)	Days[b]	Acceptable BF (Step 2) (mm)	Acceptable days (Step 3)
251-4Z	13.6	175	13.6	cull
251-5Z	14.1	166	cull	
251-6Z	15.4	160	cull	
258-4Z	10.6	182	10.6	cull
258-5Z	10.6	183	10.6	cull
258-7Z	12.5	177	12.5	cull
269-6Z	14.1	164	cull	
269-8Z	15.3	161	cull	
293-5Z[c]	13.0	168	13.0	168
293-6Z	13.8	173	13.8	cull
314-7Z	14.2	175	cull	
314-8Z	11.5	157	11.5	157
314-9Z	14.6	176	cull	
335-5Z	15.1	161	cull	
335-6Z	15.5	174	cull	
342-6Z	13.7	160	13.7	160
342-9Z	13.4	157	13.4	157

(continued)

Table 4 (*concluded*)

Gilt	BF[a] (mm)	Days[b]	Acceptable BF (Step 2) (mm)	Acceptable days (Step 3)
342-10Z	13.0	160	13.0	160
353-8Z	13.1	162	13.1	162
365-6Z	14.1	162	cull	
365-7Z	14.3	155	cull	
365-9Z	14.3	158	cull	
365-10Z	14.3	153	cull	
371-7Z	13.5	167	13.5	167
371-9Z	13.6	169	13.6	169
378-5Z	16.0	161	cull	
378-8Z	13.9	166	13.9	166
378-10Z	16.0	156	cull	
378-11Z	15.4	167	cull	
392-6Z	11.8	158	11.8	158
394-9Z	14.6	164	cull	
395-6Z	14.2	154	cull	
395-7Z	14.3	152	cull	

[a] BF = backfat thickness.
[b] Days = days to 90 kg.
[c] The 10 gilts that were selected by independent culling levels are shown in boldface.
Note: both are adjusted to 90 kg.

Therefore, out of the 33 gilts, only 10 met the standards for backfat thickness and days to 90 kg.

Independent culling levels are easy to use and have the advantage that they can be used at different stages of growth. For example the breeder could impose a minimum weaning weight for boars followed by standards for backfat thickness and days at 90 kg. However, there are two main disadvantages associated with independent culling levels:

- pigs that are good in one or more traits may be culled because of poor performance in another
- as herds change in their level of performance, for either genetic or environmental reasons, breeders must arbitrarily adjust their culling levels.

Selection index

The selection index addresses these two disadvantages of independent culling levels. It provides the means for making the most rapid improvement in the traits, by selecting for both traits at the same time. The index represents total merit, so that breeders can rank their animals from best to worst—something that is almost impossible with independent culling levels.

Though no longer in use, the old Record of Performance home-test index shows how a selection index works. The index (I) is

$$I = 100 - 17.68[(BF - \overline{BF})/\mathrm{SD}_{BF}] - 17.68[(D - \overline{D})/\mathrm{SD}_{D}]$$

where:

BF = backfat thickness, adjusted to 90 kg, of individual pig

$\overline{BF}$ = mean backfat thickness, adjusted to 90 kg, of all pigs in the herd of the same breed or cross and sex

SD_{BF} = standard deviation for backfat thickness, adjusted to 90 kg, of all pigs in the herd of the same breed or cross and sex, where standard deviation is a measure of the variation associated with backfat thickness

D = adjusted days to 90 kg of individual pig

$\overline{D}$ = mean adjusted days to 90 kg of all pigs in the herd of the same breed or cross and sex

SD_{D} = standard deviation for adjusted days to 90 kg of all pigs in the herd of the same breed or cross and sex, where standard deviation is a measure of the variation associated with days to 90 kg

17.68 = weighting factor for each trait that provides a wide range in index values to make selecting easier

100 = index for animals in the herd that are average.

Pigs having indexes greater than 100 are better than the herd average, and those with indexes less than 100 are below average. Thus, when selecting boars and gilts, choose pigs with indexes greater than 100. If the need arises to select animals having indexes below 100, choose those with indexes closest to 100.

To calculate indexes for the same group of 33 Hampshire gilts (Table 4), the means and standard deviations for adjusted backfat thickness and days to 90 kg are

	BF (mm)	*Days*
Mean	13.9	164.5
SD	1.34	8.36

Two examples of calculating indexes are shown.

Example 1 For gilt 314-8Z (11.5 mm and 157 days)

$$I = 100 - 17.68\,[(11.5 - 13.9)/1.34] - 17.68\,[(157 - 164.5)/8.36]$$
$$= 100 + 31.7 + 15.9$$
$$= 147.6$$

Example 2 For gilt 251-4Z (13.6 mm and 175 days)

$$I = 100 - 17.68\,[(13.6 - 13.9)/1.34] - 17.68\,[(175 - 164.5)/8.36]$$
$$= 100 + 4.0 - 22.2$$
$$= 81.8$$

When either the individual gilt backfat thickness or days to 90 kg is less than the mean, the index increases in value. Conversely, when either the individual gilt backfat thickness or days to 90 kg is larger than the mean, the index decreases in value. The indexes for the 33 gilts are provided in Table 5.

Table 5 Ranked indexes for 33 Hampshire gilts listed in Table 4

Gilt	Index	Rank	Gilt	Index	Rank
314-8Z[a]	147.5	1	**378-8Z**	96.8	18
392-6Z	141.5	2	**371-9Z**	94.4	19
342-9Z	122.5	3	251-5Z	94.2	20
342-10Z	121.4	4	258-7Z	92.0	21
395-7Z	121.2	5	394-9Z	91.8	22
365-10Z	119.0	6	335-5Z	91.6	23
395-6Z	118.2	7	378-10Z	90.3	24
353-8Z	115.8	8	251-6Z	89.7	25
365-7Z	114.8	9	269-8Z	88.9	26
342-6Z	112.2	10	293-6Z	83.3	27
365-9Z	108.5	11	251-4Z	81.8	28
258-4Z	106.5	12	378-5Z	79.7	29
293-5Z	104.5	13	378-11Z	74.9	30
258-5Z	104.4	14	314-7Z	73.8	31
365-6Z	102.6	15	314-9Z	66.4	32
371-7Z	100.0	16	335-6Z	58.8	33
269-6Z	98.4	17			

[a] The 10 gilts that were selected by independent culling levels are shown in boldface.

One major misconception regarding selection indexes is how the traits are weighted. The weightings used to calculate these indexes are not fixed; altering the relative weightings has a specific application. To illustrate the weighting of traits, consider the 33 Hampshire gilts. If it were more important to reduce days to 90 kg than to reduce backfat thickness, altering the relative weightings would be the best choice. The temptation is to ignore backfat completely and select solely on the basis of days to 90 kg. But, because backfat thickness and days to 90 kg are unfavorably or negatively related, reducing days to 90 kg causes backfat thickness to increase. Increasing the weighting for days to 90 kg places more emphasis on this trait but does not ignore backfat thickness. Note that as the weighting is increased on one trait relative to the other, the amount of selection pressure exerted on each trait shifts accordingly. The result of altering the relative weightings is shown using three indexes:

A = equal weighting for both traits
Weightings: *BF* = 17.68
Days = 17.68

B = 2.0 times more emphasis on days to 90 kg than on backfat thickness
Weightings: *BF* = 17.68
Days = 35.36

C = 3.0 times more emphasis on days to 90 kg than on backfat thickness
Weightings: *BF* = 17.68
Days = 53.04

Calculating the indexes results in increased values as the larger weighting is applied to days to 90 kg. What is striking is the change in the rankings of the 33 gilts for the three indexes (Table 6).

With the exception of 314-8Z (Rank = 1) and 342-6Z (Rank = 10), all gilts had their rankings either increase or decrease depending on the index used. The effect of increasing the weighting on days to 90 kg, relative to backfat thickness, is reflected in the amount of selection pressure exerted on each trait. Selection differentials, defined as the difference between the performance of the selected animals and the average for all animals, will provide the measure. Because smaller values for backfat thickness and days to 90 kg are desirable, favorable selection differentials for these traits will be negative numbers. The larger the negative number (i.e., −3.0 versus −1.5) is, the greater the selection pressure will be. To calculate selection differentials, there have to be selected animals. For this example, the top 15 Hampshire gilts under each index are used. A sample calculation of two selection differentials (Diff) for index A follows:

Average of selected gilts: backfat thickness = 13.1
days to 90 kg = 161.4

Average of all gilts: backfat thickness = 13.9
days to 90 kg = 164.5

Diff *BF* = 13.1 − 13.9 = −0.8 mm
Diff *D* = 161.4 − 164.5 = −3.1 days

The selection differentials for the three indexes are

Index	*BF (mm)*	*Days*
A	−0.8	−3.1
B	−0.1	−6.6
C	0.0	−6.8

Thus, as the weighting for days to 90 kg increases relative to backfat thickness, the selection pressure exerted on days to 90 kg increases whereas the selection pressure on backfat thickness decreases.

Table 6 Comparison of rankings for 33 gilts using three indexes

	Ranking for index				Ranking for index		
Gilt	A	B	C	Gilt	A	B	C
314-8Z	1	1	1	378-8Z	18	20	20
392-6Z	2	2	3	371-9Z	19	24	24
342-9Z	3	6	7	251-5Z	20	22	23
342-10Z	4	8	8	258-7Z	21	27	27
395-7Z	5	3	2	394-9Z	22	21	19
365-10Z	6	4	4	335-5Z	23	16	15
395-6Z	7	5	5	378-10Z	24	12	12
353-8Z	8	11	11	251-6Z	25	15	14
365-7Z	9	7	6	269-8Z	26	18	16
342-6Z	10	10	10	293-6Z	27	28	26
365-9Z	11	9	9	251-4Z	28	30	28
258-4Z	12	26	29	378-5Z	29	23	18
293-5Z	13	17	21	378-11Z	30	25	25
258-5Z	14	29	31	314-7Z	31	31	30
365-6Z	15	13	13	314-9Z	32	32	33
371-7Z	16	19	22	335-6Z	33	33	32
269-6Z	17	14	17				

EBV selection index

In 1985, the selection index based on actual measures of backfat thickness and days to 90 kg was abandoned in favor of an index that uses estimated breeding values (EBV) for both traits. The equation of this new selection index is

$$I = 100 - 17.68\,(EBV_{BF}/\mathrm{SD}_{EBV_{BF}}) - 17.68\,(EBV_{D}/\mathrm{SD}_{EBV_{D}})$$

where:

EBV_{BF}	=	estimated breeding value for backfat thickness
$\mathrm{SD}_{EBV_{BF}}$	=	standard deviation of estimated breeding value for backfat thickness
EBV_{D}	=	estimated breeding value for days to 90 kg
$\mathrm{SD}_{EBV_{D}}$	=	standard deviation of estimated breeding value for days to 90 kg
17.68	=	weighting factor for each trait that provides a wide range in index values to make selecting easier
100	=	index of animals in the herd that are average.

Estimated breeding values use the backfat thickness and days to 90 kg of each animal along with other information that includes

- heritability or degree of inheritance associated with each trait
- backfat thickness and days to 90 kg that are available on all relatives (i.e., sire, dam, grandparents, siblings, and so on)
- genetic merit of the herd
- any genetic change that has occurred in the breed in a particular region of the country (i.e., the four regions being the West, Ontario, Quebec, and the Atlantic Provinces). The accuracy of a pig's EBV is related to how much information is available on its relatives. The greater the amount of information there is, the greater the accuracy will be. This accuracy is called the repeatability of the EBV.

To calculate the EBV selection index, the standard deviations of the EBVs for backfat thickness and days to 90 kg need to be known. The values for these parameters in Ontario are 1.1 and 3.9 for backfat thickness and days to 90 kg, respectively. Thus, the indexes for two pigs (A and B) in Ontario, for example, with EBVs of −2.2 and −2.1 for backfat thickness and −21.2 and −20.4 for days to 90 kg, respectively, are calculated as follows:

$$\begin{aligned} I_A &= 100 - 17.68(-2.2/1.1) - 17.68(-21.2/3.9) \\ &= 100 + 35.4 + 96.1 \\ &= 231.5 \end{aligned}$$

$$I_B = 100 - 17.68(-2.1/1.1) - 17.68(-20.4/3.9)$$
$$= 100 + 33.7 + 92.5$$
$$= 226.2$$

Selecting boars using the EBV index is no different than using an index based on actual measures of backfat thickness and days to 90 kg. The larger the index value is, the better the animal is expected to be. Thus, in the Ontario example, pig A would be ranked higher ($I_A = 231.5$) than pig B ($I_B = 226.2$). The relative weightings for the two traits can be altered to place more emphasis on either trait. The only requirement is that the breeder has values for the standard deviation of the EBVs for that particular region of the country. The standard deviation can be obtained from

Agriculture Canada
Livestock Development Branch
Sir John Carling Building
Ottawa, Ont. K1A 0C5

One concern regarding the use of EBVs is that they have only been evaluated by computer simulation (i.e., one computer program evaluating another computer program). Based on these evaluations, the EBVs have proven better than selection based on actual measures of backfat thickness and days to 90 kg. However, until the procedures have been examined in a living population (of pigs or mice) under controlled conditions, this concern will persist.

Sow productivity and management program

The function of this new computer program is to provide breeders, of both purebred and commercial animals, with a record-keeping system for sow productivity. The records gathered will provide guidelines for breeders to improve management and increase selection for reproductive traits. This information will result in a database that can be used to assess sow productivity in Canada. Sow productivity data have been collected for several years but the new aspect of the program is the calculation of EBVs for these traits. The procedure for calculating these EBVs is currently being evaluated by Agriculture Canada (Livestock Development Branch) and is expected to be fully operational in the near future.

Crossbreeding

Before examining crossbreeding systems for their practicality, it is necessary to review the concept of crossbreeding. Crossbreeding is simply defined as the mating of animals from two different breeds.

Major reasons for crossbreeding are

- the beneficial effect of heterosis or hybrid vigor
- the combination of desirable characteristics of two or more breeds.

Hybrid vigor is the difference in performance between crossbred offspring and the average performance of the parental breeds that make up the cross. For example, consider the cross of boars from breed A with sows from breed B. Suppose the average litter size and piglet weaning weight in breeds A, B, and AB are

Breed or cross	*Litter size*	*Weaning weight* (kg)
A	10.2	6.6
B	9.0	9.0
AB	10.0	8.0

The average of the parental breeds (A and B) are 9.6 for litter size and 7.8 kg for weaning weight. Thus, the actual hybrid vigor for litter size is 0.4 piglets and 0.2 kg for weaning weight. On a percentage basis, these hybrid vigor levels represent 4.2% for litter size and 2.6% for weaning weight. Percent hybrid vigor is actually hybrid vigor expressed as a percentage of the parental average. This example also shows the two reasons for crossbreeding:

- improving performance through hybrid vigor
- combining the litter size of breed A with the heavier weaning weight of breed B.

The major benefits of hybrid vigor are found in the lowly heritable traits, those associated with reproduction and fitness. In the section entitled "Inbreeding," you will read that inbreeding depression is greatest in these same types of traits. In fact, hybrid vigor and inbreeding are exact opposites. Hybrid vigor results in less homozygosity (the tendency of genes at all locations on the chromosomes to be the same) and greater heterozygosity (the tendency of genes at all locations on the chromosomes to be different), whereas inbreeding leads to greater homozygosity and less heterozygosity. Hybrid vigor can be expressed in two ways: individual and maternal. Individual hybrid vigor is the greater vigor and reduced mortality of crossbred piglets, and maternal hybrid vigor is the increased litter performance of crossbred sows. Table 7 shows the circumstances in which these forms of hybrid vigor would be present.

Table 7 The expression of hybrid vigor

		Hybrid vigor	
Sire[a]	Dam	Individual	Maternal
Y	Y	no	no
Y	L	yes	no
H	YL	yes	yes
DH	Y	yes	no

[a] Y = Yorkshire, L = Landrace, H = Hampshire, D = Duroc.

In a review of crossbreeding experiments conducted in the United States and Canada, Dr. Rodger Johnson, of the University of Nebraska at Lincoln, summarized percent individual and maternal hybrid vigor of all breed crosses studied for several traits (Table 8).

Table 8 Estimates of individual and maternal hybrid vigor

	Hybrid vigor (%)	
Trait	Individual	Maternal
Ovulation rate	0.3	–
Conception rate	3.8	–
Litter size		
birth	1.0	4.7
21 days	8.0	8.7
weaning	10.1	7.7
Pig weight		
birth	3.1	1.5
21 days	3.1	3.7
weaning	4.8	8.2
Postweaning		
daily gain	9.4	0.0
feed efficiency	2.3	0.0
Age at 100 kg	6.5	1.2
Carcass length	0.0	0.2
Carcass backfat	2.5	4.4
Loin eye area	1.8	0.4

Source: after Johnson, R.K. 1980. Heterosis and breed effects in swine. North Central Regional Publication No. 262.

There are two main types of crossbreeding systems from which producers can choose: terminal and rotational. The major differences are that

- all progeny from terminal systems are destined for market
- terminal systems also allow for maximum individual (except the backcross) and maternal (except the single cross) hybrid vigor.

Terminal crossbreeding

There are four major plans: the single cross, the backcross, the three-breed cross, and the four-breed cross.

Single cross

The single cross, which produces F_1 pigs, is the basis of all crossbreeding systems, regardless of whether they are terminal or rotational systems:

Breed of sire × *dam*	*Genetic make-up of offspring* (F_1)
A × B	50% A, 50% B

Advantages

- herd has 100% individual pig hybrid vigor
- once the two breeds have been selected, the breeding plan is quite simple.

Disadvantages

- herd has no maternal hybrid vigor as the sows are all purebred
- producers have to purchase replacement gilts and rely on someone else's breeding program to produce high-quality gilts.

Backcross

Backcross pigs are the result of two crosses (A × B to produce AB gilts and then A × AB to produce 75% A, 25% B or backcross pigs):

Breed of sire × *dam*		*Genetic make-up of offspring* (backcross)
A × AB		75% A, 25% B
	or	
B × AB		25% A, 75% B

Advantages

- 100% maternal hybrid vigor
- 50% individual pig hybrid vigor.

Disadvantages

- herd has 50% less individual pig hybrid vigor
- producers have to purchase replacement gilts and rely on someone else's breeding program to produce high-quality gilts.

Three-breed cross

A three-breed cross combines a breed that produces a good carcass (breed C) with a crossbred female that reproduces exceptionally:

Breed of sire × dam	*Genetic make-up of offspring*
C × AB	50% C, 25% A, 25% B (go to market)

Advantages

- 100% maternal hybrid vigor
- 100% individual pig hybrid vigor.

Disadvantage

- producers have to purchase replacement gilts and rely on someone else's breeding program to produce high-quality gilts.

Four-breed cross

A four-breed cross combines two breeds that produce a good carcass (breeds C and D) with a crossbred female that reproduces exceptionally:

Breed of sire × dam	*Genetic make-up of offspring*
CD × AB	25% C, 25% D, 25% A, 25% B (go to market)

Advantages

- 100% maternal hybrid vigor
- 100% individual pig hybrid vigor
- 100% paternal hybrid vigor for mating behavior (libido) and fertility.

Disadvantage

- producers have to purchase replacement gilts and rely on someone else's breeding program to produce high-quality gilts.

Rotational crossbreeding

There are two major plans: the two-breed or crisscross rotation and the three-breed rotation.

Two-breed or crisscross rotation

Year	*Breed (cross) of sire × dam*	*Genetic make-up of offspring*	
1	A × B	50% A, 50% B	(1)
2	B × (1)	25% A, 75% B	(2)
3	A × (2)	62.5% A, 37.5% B	(3)
4	B × (3)	31.25% A, 68.75% B	(4)
5	A × (4)	65.625% A, 34.375% B	(5)

After a few more years, the composition of the offspring will stabilize such that two-thirds (67%) of the breed composition will be the sire breed and one-third (33%) will be the other breed.

Advantages

- herd has 67% individual pig and maternal hybrid vigor
- replacement females are produced and not purchased
- producers must keep accurate records to keep track of which sire breeds to use.

Disadvantage

- herd loses 33% of the individual pig and maternal hybrid vigor.

Three-breed rotation

Year	*Breed (cross) of sire × dam*	*Genetic make-up of offspring*	
1	A × B	50% A, 50% B	(1)
2	C × (1)	50% C, 25% A, 25% B	(2)
3	A × (2)	25% C, 62.5% A, 12.5% B	(3)
4	B × (3)	12.5% C, 31.25% A, 56.25% B	(4)
5	C × (4)	56.25% C, 15.625% A, 28.125% B	(5)
6	A × (5)	28.125% C, 57.8125% A, 14.0625% B	(6)

Advantages

- herd has 86% individual pig and maternal hybrid vigor
- replacement females are produced and not purchased
- producers must keep accurate records to keep track of which sire breed to use.

Disadvantage

- herd loses 14% of the individual pig and maternal hybrid vigor.

Not one of the crossbreeding systems described here is ideal for all situations. The perfect crossbreeding system would maximize individual pig and maternal hybrid vigor and would allow for the simple production of replacement gilts. A possibility that is worth exploring is to combine the two-breed rotation and the three-breed terminal systems. Under this hybrid system, the two-breed rotation would be used to produce the replacement gilts and those females not used to produce replacement gilts would be bred to a third breed.

Consider the following situation: from a 100-sow herd, every year 20 sows are culled. Assume the following:

- four gilts are weaned per litter
- the producer grows out 40 gilts and selects the best 20 every year as potential replacements.

The 40 gilts needed by the producer for performance testing represent the litters of 10 sows. These 10 sows are actually the two-breed rotation herd; the remaining 90 sows can be bred to a third breed to produce market pigs. Production of pigs under this system of crossbreeding would be as follows:

Phase 1 Two-breed rotation

Sows	*Breed composition*	*Gilts*
10	75% A, 25% B or 25% A, 75% B	40

Note: the best 20 gilts are potential replacement gilts and the remaining 20 gilts are sold.

Phase 2 Three-breed terminal cross

Sows	*Breed composition*	*Pigs*
90	50% C, 37.5% A, 12.5% B or 50% C, 12.5% A, 37.5% B	720

Note: the 720 pigs represent one farrowing per sow and all go to market.

Advantages

- herd has 100% individual pig hybrid vigor
- herd has 67% maternal hybrid vigor
- replacement females are produced and not purchased
- producers must keep accurate records to keep track of which sire breed to use.

Disadvantages

- herd loses 33% of the maternal hybrid vigor
- producers have to maintain purebred boars or use AI, or both.

A variation of this plan would be to purchase purebred gilts of breed A and cross them to boars of breed B to produce crossbred gilts that are crossed to a terminal sire breed. Initially, the producer would have to purchase either crossbred gilts or make sufficient A $\times$ B matings to establish the crossbred component of the herd. Once the crossbred component becomes operational, the purchased gilts (breed A) mated to breed B would provide replacement gilts for the crossbred component. Using a 100 sow example:

Phase 1 Single cross

Sows	*Breed composition*	*Gilts*
10	50% A, 50% B	40

Note: (1) the best 20 gilts are potential replacements and the remaining 20 gilts are sold; and (2) the purebred gilts in this component would be purchased from an external source.

Phase 2 Three-breed terminal cross

Sows	*Breed composition*	*Pigs*
90	50% C, 25% A, 25% B	720

Note: the 720 pigs represent one farrowing per sow and all go to market.

Advantages

- herd has 100% individual pig and maternal hybrid vigor
- replacement gilts represent a small proportion of the herd
- producers must keep accurate records to keep track of which sire breed to use.

Disadvantage

- none.

Genetic lag

A factor that is often overlooked when crossbreeding systems are being considered is genetic lag, which is the amount of time required for genetic improvement to be expressed in the market pigs. Genetic lag is affected by the following:

- performance testing of boars and gilts—selection for breeding of above-average animals decreases genetic lag; conversely, the choice of below-average animals increases genetic lag
- proportion of boars (or semen) purchased versus proportion of boars that are produced on the farm—as the proportion of purchased boars (or semen) decreases, genetic lag increases, and vice versa
- longevity of boars and gilts in the herd—the longer boars and gilts are retained for breeding, the longer will be the genetic lag; whereas, the shorter the time that boars and gilts are retained for breeding, the shorter the genetic lag
- purchase of replacement females—purchasing replacement females decreases genetic lag.

Given these points, genetic lag can be minimized by purchasing all above-average animals from performance-tested herds, and keeping

them for only one breeding. Although this action would minimize genetic lag, it would probably not be practical. Commercial crossbreeding programs are designed to produce a quality hog that maximizes profit. To do this, producers use

- genetics to improve the growth and carcass attributes of the market pigs
- sows to increase the number of market pigs
- crossbreeding system, either terminal or rotational, to best suit their needs and operation.

With the present carcass grading system in Canada, which encourages leanness, and the importance of minimizing time spent in the grower–finisher barn, the use of performance-tested animals is essential. The issue of purchased boars versus boars produced on the farm is probably a nonissue because most commercial producers rely on purebred breeders or AI studs, or both, for their boar power. Longevity of boars and gilts in the commercial herd is a definite issue. There is a trade-off between genetic improvement and productivity—each has its merits. As a rule of thumb, cull a sow as soon as her productivity decreases or the performance of her offspring (i.e., days to reach market weight or grade index) decreases relative to the offspring of other sows. This last point can be used to determine when a boar has reached the limit of his effectiveness. Purchasing replacement females depends on the type of crossbreeding system used. A terminal system requires that replacement gilts be purchased and has a shorter genetic lag than a rotational system that produces its own replacement gilts. Note that, under a rotational system, longevity in the herd and a stringent performance-testing program can reduce the difference in genetic lag between the terminal and rotational systems.

Regardless of the crossbreeding system or the breeds involved, the one factor that must be considered is the quality of the breeding stock. For crossbreeding to be effective, the breeding stock has to be of high quality.

Purchasing boars is easier than replacement gilts because of the options available. High-quality boars can be purchased "in the flesh" or in the form of semen; probably the best system is to use both live boars and semen. If semen is used, the producer can incorporate superior breeding into the herd that would not be readily available by directly purchasing boars.

If the crossbreeding system in use requires buying replacement gilts, purebred or crossbred, the producer must be selective. Finding a source of high-quality gilts that are performance-tested and produced under an intensive selection program is essential. In a rotational system, it is the responsibility of the producer to have an active selection program with definite goals: lower backfat levels and improved growth rate. The use of inferior breeding stock in a crossbreeding program will result in lower carcass indexes and more time spent in the finishing barn.

Genetic defects and abnormalities

A pig, like all living organisms, is the product of its genetic make-up (or genotype) and the environment in which it lives. Within the genotype, not only are there genes that can make a pig very good or very poor, but there are also genes that can cause death or impair the animal. Genetic defects and abnormalities are produced by those genes that cause death, called lethal genes, or impair, called nonlethal deleterious or sublethal genes. There are some genetic mechanisms that show how these types of genes are expressed. The most common is the simple recessive.

Recessive genes

Simple recessive genes cause the following defects:

bent legs (lethal) Legs are bent at a right angle and stiff; most common in the front legs but rear legs may also be affected.

brain hernia (lethal) Skull does not completely close, and the brain protrudes covered only by a membrane.

catlin mark (lethal) Incomplete skull development.

cleft palate (lethal) The palate does not close during development.

excessive fatness (lethal) Pigs become very fat between 30 and 70 kg liveweight and die.

hemophilia (lethal) Pigs have a normal appearance but bleed to death from slight wounds.

hydrocephalus (lethal) Fluid build-up on the brain causing an enlargement of the head; fluid interferes with bone growth of the head.

muscle contracture (lethal) Forelegs are stiff.

paralysis (lethal) Hind legs are paralyzed.

leglessness or "streamlined" (lethal) Pigs are born with no legs and soon die.

thickened forelimbs (lethal) Swollen forelimbs produced by gelatinous infiltration of connective tissue replacing muscle.

eyes absent (partially lethal) No eyes in the sockets.

kinky tail (nonlethal deleterious) Rigid angles in the tail, and the rigidity increases as the pigs get older; afflicted pigs have a high incidence of abnormal kidneys, ureters, and genitalia.

melanotic tumors (nonlethal deleterious) Moles or skin tumors that are small at birth but enlarge with age; moles are heavily pigmented and contain hair (Note: not all moles are genetic).

For any of these defects to occur the pig must possess two copies (i.e., be homozygous) of the recessive genes at the same chromosome location.

To illustrate this consider the example of paralysis. Let P be the normal and dominant gene and p be the recessive gene for paralysis. Because this defect is a lethal condition, there are no pp genotypes in the herd, and the PP and Pp genotypes cannot be separated. Pigs that carry a recessive defect that is masked by the dominant gene are called carriers. The matings possible during the breeding season are listed in Table 9.

Table 9 Consequences of a recessive gene for paralysis in a breeding herd

Sire × Dam	Offspring	Phenotype
PP × PP	100% PP	100% normal
× Pp	50% PP, 50% Pp	100% normal
Pp × PP	50% PP, 50% Pp	100% normal
× Pp[a]	25% PP, 50% Pp, 25% pp	75% normal, 25% die

[a] Only the mating of a boar and sow that carry both the P and p genes will produce pp piglets that die.

If we consider a nonlethal defect, like kinky tail, the situation differs somewhat. Let K be the dominant and normal gene and k be the recessive gene for kinky tail. The possible matings are listed in Table 10.

Table 10 Consequences of a recessive gene for kinky tail in a breeding herd

Sire × Dam	Offspring	Phenotype
KK × KK	100% KK	100% normal
× Kk	50% KK, 50% Kk	100% normal
× kk	100% Kk	100% normal
Kk × KK	50% KK, 50% Kk	100% normal
× Kk	25% KK, 50% Kk, 25% kk	75% normal, 25% kinky tail
× kk	50% Kk, 50% kk	50% normal, 50% kinky tail
kk × KK	100% Kk	100% normal
× Kk	50% Kk, 50% kk	50% normal, 50% kinky tail
× kk	100% kk	100% kinky tail

As in the example on paralysis, each parent must have at least one recessive gene for the defect to be expressed. However, the possibilities for keeping the gene in the herd are greatest with nonlethal deleterious defects because both heterozygous (Kk) and homozygous recessive (kk) animals preserve the gene.

Double recessive genes (i.e., recessive genes at two different locations on a chromosome) cause the following defects:

hairlessness (nonlethal deleterious) A condition in which there are few normal hair follicles.

stringhalt (nonlethal deleterious) Characterized by pigs lifting the leg with a jerk, and, in extreme instances, the leg going as high as the back.

To visualize how these defects come about, consider H as the normal and dominant gene for hair and h as the hairless and recessive gene at the first location, and consider B as the normal and dominant gene for hair and b the hairless and recessive gene at the second location. The possible genotypes for these genes are

Genotype	*Result*
HHBB	hair
HHBb	hair
HHbb	hair
HhBB	hair
HhBb	hair
Hhbb	hair
hhBB	hair
hhBb	hair
hhbb	hairless.

Only the totally recessive genotype (hhbb) produces the hairless condition. With the exception of the HHBB and hhbb genotypes, the remaining genotypes are all carriers for the defect. The number of recessive genes range from one to three for these carriers. It is evident that only matings which involve the HhBb, Hhbb, hhBb, and hhbb genotypes would produce hairless pigs. The percentages of hairlessness in the offspring resulting from mating these genotypes is as follows:

Sire	× *Dam*	*Hairlessness(%)*
HhBb	× HhBb	6.25
	× Hhbb	12.5
	× hhBb	12.5
	× hhbb	25.0
Hhbb	× Hhbb	25.0
	× hhBb	25.0
	× hhbb	50.0
hhBb	× hhBb	25.0
	× hhbb	50.0
hhbb	× hhbb	100.0

The highest incidences of hairlessness result from mating boars or sows exhibiting hairlessness.

Dominant genes

Dominant genes can also produce defects. The following are examples of defects caused by a dominant gene at the same location on a chromosome:

umbilical hernia (nonlethal deleterious) A weakness in the belly wall at the navel or bellybutton that allows the intestines to protrude.

syndactyly or mule foot (nonlethal deleterious) Only one toe develops instead of two.

wattles (nonlethal deleterious) Skin-like flaps that hang from the throat near the lower jaw.

woolly (nonlethal deleterious) Kinky hair.

Any of these conditions need only one dominant gene to be expressed in a pig, in contrast to defects caused by recessive genes at one location on a chromosome. To demonstrate this point, let W represent the dominant gene that causes wattles and w represent the normal gene. Wattles occur when the pig has either WW or Ww as a genotype, and normal pigs have the ww genotype. Making all possible matings of these genotypes would produce the following:

Sire	× *Dam*	*Offspring*	*Wattles %*
WW	× WW	100% WW	100
	× Ww	50% WW, 50% Ww	100
	× ww	100% Ww	100
Ww	× WW	50% WW, 50% Ww	100
	× Ww	25% WW, 50% Ww, 25% ww	75
	× ww	50% Ww, 50% ww	50
ww	× WW	100% Ww	100
	× Ww	50% Ww, 50% ww	50
	× ww	100% ww	0

With this type of inheritance, it is easy to cull afflicted pigs from the herd because the defective gene is expressed at all times.

The final known genetic cause involves dominant genes at two different locations on a chromosome. An example of this is

whorls (nonlethal deleterious) The appearance of the hair is affected.

To get a feel for this type of inheritance, the possible genotypes must be studied.

Let S be the dominant gene that causes whorls at location 1
s be the normal gene at location 1
L be the dominant gene that causes whorls at location 2
l be the normal gene at location 2.

The possible genotypes are

Genotype	*Result*
SSLL	whorl
SSLl	whorl
SSll	normal
SsLL	whorl
SsLl	whorl
Ssll	normal
ssLL	normal
ssLl	normal
ssll	normal

Of the five genotypes that did not produce whorls, four (SSll, Ssll, ssLL, and ssLl) are carriers for the defect because the dominant genes required for expression of the trait are preserved.

The final grouping of defects are those that are suspected of having a genetic cause, but the mechanism has not yet been found. Traits in this group include:

atresi ani (lethal) There is no anal opening; it causes death in males; females void feces through the vulva.

ear defect (lethal) The ears are split, and the rear legs are twisted.

inverted nipples (nonlethal deleterious) The teats turn inward instead of protruding outward so that the piglets cannot nurse.

mastitis (nonlethal deleterious) Caked udders that may have to be removed to save the sow; this condition occurs in certain strains.

polydactyly (nonlethal deleterious) Extra toes on the front feet.

myoclonia congenita or "shakers" (nonlethal deleterious) Piglets born that tremble; the severity ranges from slight shivering to severe shaking, making it difficult for the piglet to suckle a teat.

splay leg (nonlethal deleterious) Newborn piglets are unable to stand or walk because the legs (usually the hind legs) are splayed out to the side or the front; certain breeds and strains are more likely to express the trait.

hermaphrodites or pseudo-hermaphrodites (nonlethal deleterious) Hermaphrodites have tissue from the testes and ovary present; pseudo-hermaphrodites have testes tissue (but no ovary tissue) and secondary female sex organs (vulva, vagina, and uterus).

cryptorchidism (nonlethal deleterious) A sex-limited trait where one or both of the testes fail to descend normally into the scrotum.

scrotal hernia (nonlethal deleterious) A sex-limited trait where the muscles of the inguinal ring are weakened and the intestines pass into the scrotum.

Regardless of the mechanism that causes cryptorchidism and scrotal hernia, the expression of the trait depends upon the sex of the pig. If the

mechanism is present and the pig is a male, then the trait is expressed; if the pig is a female then the trait is not expressed.

Halothane gene

Though not considered a genetic defect like those already discussed, the halothane gene is the cause of porcine stress syndrome (PSS). This syndrome is described as the sudden and unexpected death of pigs during transportation of normal daily activities, such as exercise or fighting. Related to PSS is malignant hyperthermia (MH), which is the uncrontrollable increase in body temperature that kills the pig. Closely associated with MH is pale, soft, and exudative (PSE) pork. Note that PSE pork is not completely caused by genetics. The method of handling the pigs immediately prior to slaughter and the carcasses immediately after slaughter can influence the incidence of PSE pork.

The genetic mechanism that produces PSS is a recessive gene generally referred to as the halothane gene. It has that name because exposing a pig to halothane gas, an anaesthetic, is the method of identifying PSS and nonPSS pigs. The halothane test is quite simple. Pigs breathe halothane for no more than 5 min. If a pig's muscles become rigid, then the pig is called either a reactor or halothane-positive and is stress-susceptible. Pigs that relax and go to sleep are called nonreactors or halothane-negative. Designating the halothane gene as n and the normal, dominant gene as N, the possible genotypes are

Genotype	*Halothane reaction*	*Stress-susceptible*
NN	Negative	No
Nn	Negative	No
nn	Positive	Yes

Thus the halothane test can be used to identify pigs that are stress-susceptible, but the problem is the heterozygote (Nn) or carrier. A considerable research effort is under way to identify carrier pigs by means of genetic and physiological markers. Genetic or gene markers are genes that are closely associated or linked with the halothane gene. These are used to accurately predict the presence of the halothane gene in either the nn or Nn genotypes. Physiological markers are chemical properties that can be attributed to the presence of zero, one, or two halothane genes. Characterizing these properties would also be used to identify the nn and Nn genotypes.

Research has shown that halothane-positive or stress-susceptible pigs differ from halothane-negative pigs for reproductive, performance, and carcass traits. Generally, the halothane gene leads to an increased lean yield of the carcass and reduced litter size at birth and weaning. It has also been associated with reduced backfat thickness, growth rate, and feed efficiency though there is considerable evidence to support or contradict these relationships.

Jones and co-workers gave a more detailed description of the genetics of PSS in the Agriculture Canada Technical Bulletin 1988-11E entitled *Pork quality: a technical review.* Copies of this publication, prepared by the Red Meats Group at the Agriculture Canada Research Station in Lacombe, Alta., can be obtained by writing to

Director
Research Station
Research Branch, Agriculture Canada
Bag Service 5000
Lacombe, Alta. T0C 1S0

Defects and the breeding herd

The most practical recommendation regarding defects in a breeding herd is to cull the animal. If the defect has no known genetic cause, do not take a chance—cull. In litters in which the incidence of the defect is less than 20%, culling the individual pig is effective; when the incidence is greater than 20%, culling the littermates is in order. If the entire litter is affected by a defect, then cull both the sire and the dam. If that culled boar sired other litters, then monitor the offspring as well as any offspring they may have. Selection against a defect cannot completely eliminate that defect from a herd or population. As the frequency of the defective gene becomes smaller and smaller, it will eventually equal the mutation rate—the rate at which the gene causing the defect is produced by mutation. When gene frequency equals the mutation rate, every defective gene that is eliminated by selection is replaced by another defective gene produced by mutation.

Inbreeding

Inbreeding is the mating of animals related to each other more closely than the average of the herd. This process reduces the number of gene pairs that have different or heterozygous alleles and increases the number of gene pairs with alike or homozygous alleles. Shifting a population towards increased homozygosity by inbreeding produces effects similar to selection, except that in selection the shift is towards the favorable genes. With inbreeding the shift is completely by chance; that is, the homozygous gene pairs that accumulate can either be favorable or unfavorable with equal probability.

An increase in homozygosity, as a result of inbreeding, can lead to an increased expression of genetic defects. However, the more serious problem is inbreeding depression, which is the decreased performance of traits as inbreeding levels increase; it is most evident in traits associated with fertility, survival, and size. In 1968, two examples from research in the United States by Bereskin and co-workers showed that for every 10% increase in inbreeding, the number born alive decreases by about 0.24

piglets and body weight is 2.6 kg less at 154 days of age. Inbreeding depression is subtle in its expression. If producers do not monitor the inbreeding levels in their herds, these effects are often attributed to disease, feeding, and seasonal conditions.

To monitor inbreeding levels, producers must be able to calculate the inbreeding coefficient for any or all of their pigs. The inbreeding coefficient, defined as F, is the chance that a gene present in a pig came from the same distant relative. This definition provides the basis for the presence or absence of inbreeding: the need for an ancestor that appears on the sire or paternal side and the dam or maternal side of the pedigree.

Calculation of inbreeding coefficients

Step 1 Identify the sire and dam that are to breed, and write out their respective complete pedigrees.

Step 2 Draw a line through the middle of the pedigree to separate the paternal and maternal sides of the pedigree. Scan both sides of the pedigree starting from the left-hand side and proceeding to the right to find ancestors that appear on both the paternal and maternal sides. Such ancestors are called common ancestors, and inbreeding can only exist if there are common ancestors.

Step 3 Determine if the common ancestors are inbred. To do this, the pedigree of the common ancestors must be examined following the same method described in step 2.

Step 4 Calculate the degree of inbreeding associated with the offspring (F_x).

(i) Trace the genetic contribution of the common ancestors on both the paternal and maternal sides of the pedigree.

(ii) Calculate the preliminary inbreeding level due to the common ancesters(F_p).

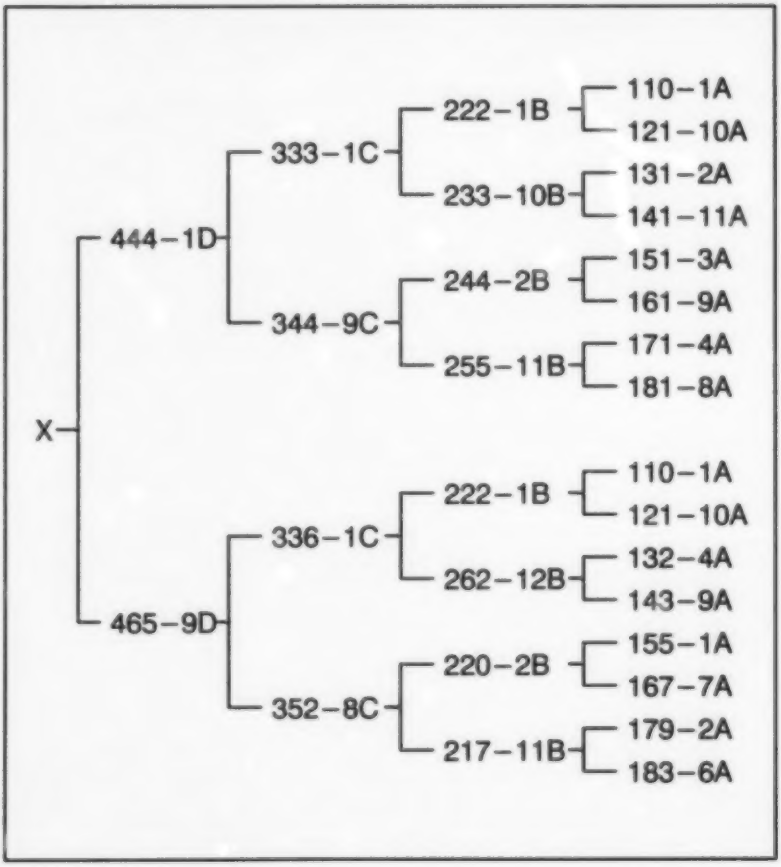
(iii) Combine F_p with the degree of inbreeding of the common ancestors (F_{ca}) to obtain the actual inbreeding level resulting from the common ancestors (F_a).

(iv) Finally, add the actual inbreeding levels (F_a) of each common ancestor to calculate the inbreeding level (F) of the animal in question.

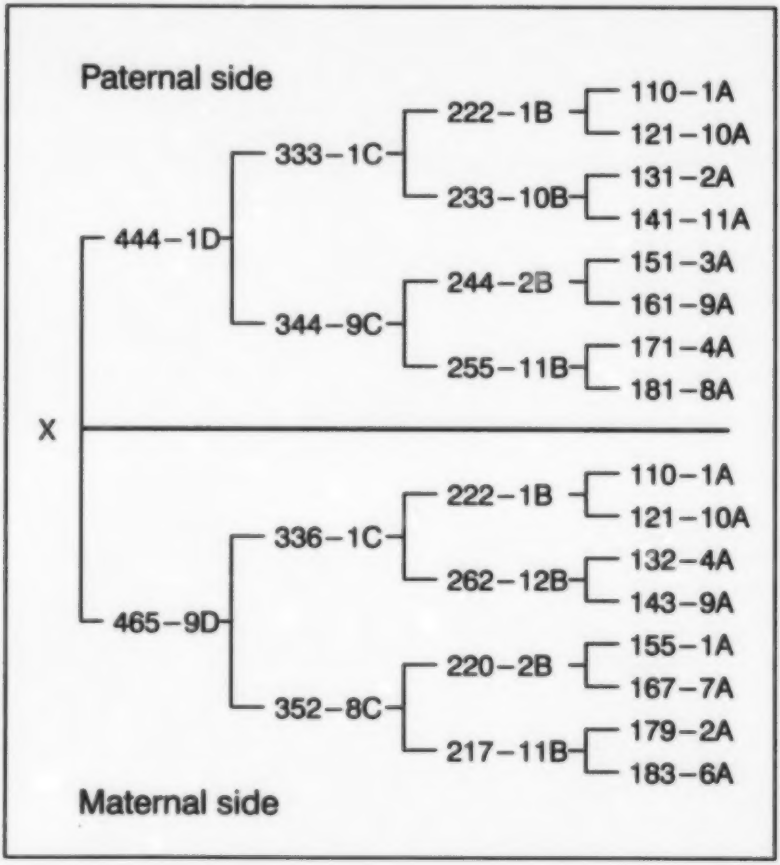
Example 1

A swine breeder wants to mate his best boar (444-1D) to a recently purchased gilt (465-9D).

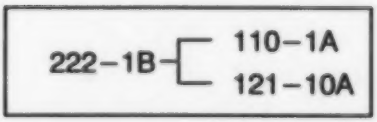
Step 1 The pedigree for the offspring X produced by 444-1D and 465-9D is



Step 2 In this pedigree, the only common ancestor is 222-1B. The sire and dam of this animal (i.e., 110-1A and 121-10A) are not considered common ancestors because their genetic contribution is accounted for by 222-1B.



Step 3 the pedigree of 222-1B is



Clearly, 222-1B is not inbred based on the information supplied by the pedigree. Only the sire and dam of 222-1B are listed and there is no indication that they are related.

Step 4(i)

Paternal trace The animals between the common ancestor and X are 333-1C and 444-1D. Thus, the number of animals between the common ancestor and X on the paternal side (n_p) is 2.

Maternal trace The animals between X and the common ancestor are 465-9D and 336-1C. Thus the number of animals between X and the common ancestor on the maternal side (n_m) is 2.

Step 4(ii) The preliminary inbreeding coefficient due to 222-1B is

$$F_p = (0.5)^{n_p + n_m + 1}$$

In this equation, 0.5 is the chance of a particular gene being passed from parent to offspring; n_p+n_m+1 converts the chance of a particular gene being passed from parent to offspring to the chance of a gene being passed from the common ancestor to X. The n_p and n_m terms refer to the number of animals in the paternal and maternal traces, respectively, and adding 1 to the sum of n_p and n_m has a corrective purpose. Thus,

$$F_p = (0.5)^{2+2+1} = (0.5)^5$$
$$= 0.03125$$

(Note: See inside the back cover for exponential values that will aid in these calculations.)

Step 4(iii) Combining F_p with the inbreeding of the common ancestor (F_{ca}) to obtain the actual inbreeding level (F_a) is

$$F_a = F_p \times (1 + F_{ca})$$

Since 222-1B is not inbred,

$$F_a = 0.03125 \times (1 + 0)$$
$$= 0.03125$$

Step 4(iv) The actual inbreeding for all common ancestors, in this case only one, shows that the amount of inbreeding for X (F_x) is

$$F_x = F_a = 0.03125 \text{ or } 3.125\%$$

Thus, the chance of animal X having received a particular gene from 222-1B is 3.125% (Table 11).

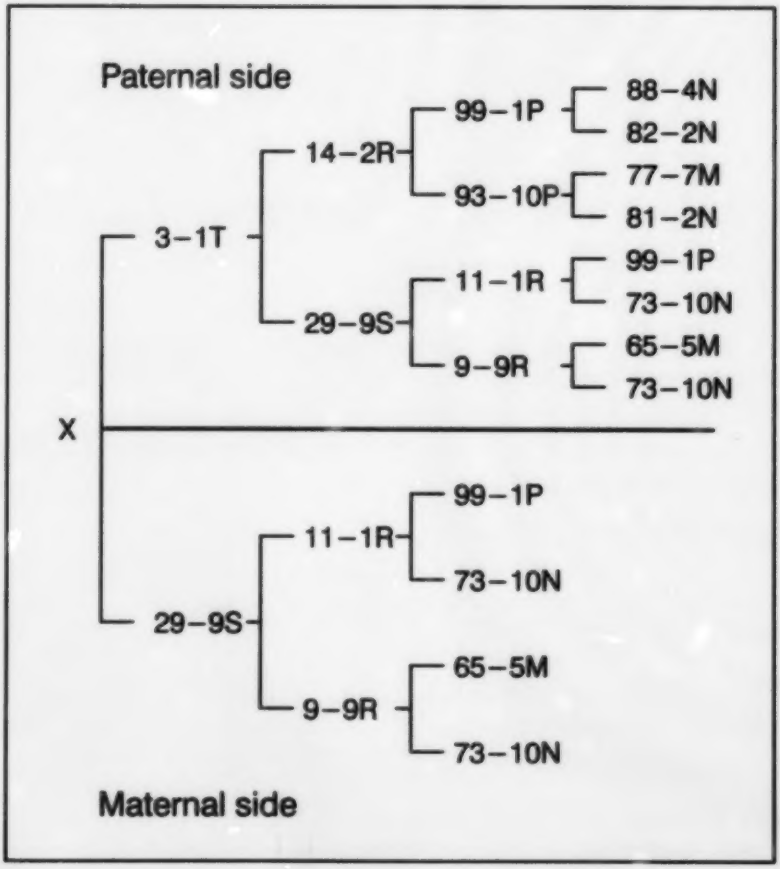
Table 11 Calculation of the inbreeding level for piglet X

Common ancestor	n_p	n_m	+1	F_p	$(1 + F_{ca})$	F_a
222-1B	2	2	1	$(0.5)^5$	1 + 0	0.03125
					$F_x =$	0.03125
						or 3.125%

Example 2

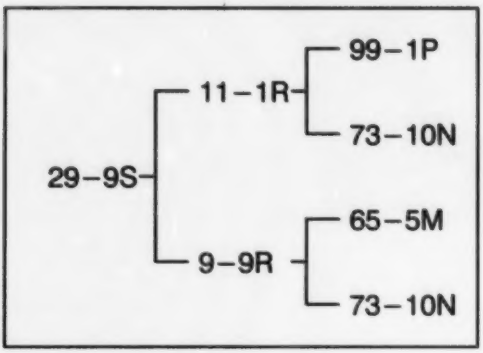
The pedigree for piglet Y is presented to familiarize the reader with the steps in determining its level of inbreeding.

Step 1 The given pedigree is represented below; proceed to step 2.



Step 2 The most obvious common ancestor is 29-9S, but 99-1P is also a common ancestor. The reason that 99-1P is a common ancestor is because its influences come through 14-2R and 3-1T on the paternal side to piglet Y and through 11-1R and 29-9S on the maternal side to piglet Y. This type of common ancestor is often missed, and it stresses the importance of tracing the genetic contribution of common ancestors and potential common ancestors.

Step 3 In determining if the common ancestors are inbred, no pedigree information is available on 99-1P. Thus, we have to assume that this boar is not inbred. However, there is pedigree information available on 29-9S.



Scanning the pedigree of 29-9S there is only one common ancestor, 73-10N, and we must assume that this sow is not inbred as there is no pedigree information available on it.

Paternal trace 11-1R is between 73-10N and 29-9S, $n_p = 1$.
Maternal trace 9-9R is between 29-9S and 73-10N, $n_m = 1$.

The inbreeding level of 29-9S is

$$(0.5)^{1+1+1} = (0.5)^3$$
$$= 0.125 \text{ or } 12.5\%$$

Step 4 Calculate the inbreeding of piglet Y (Table 12).

For common ancestor 29-9S:

Paternal trace 3-1T is between 29-9S and Y, $n_p = 1$.
Maternal trace no animals are between Y and 29-9S, $n_m = 0$.

For common ancestor 99-1P:

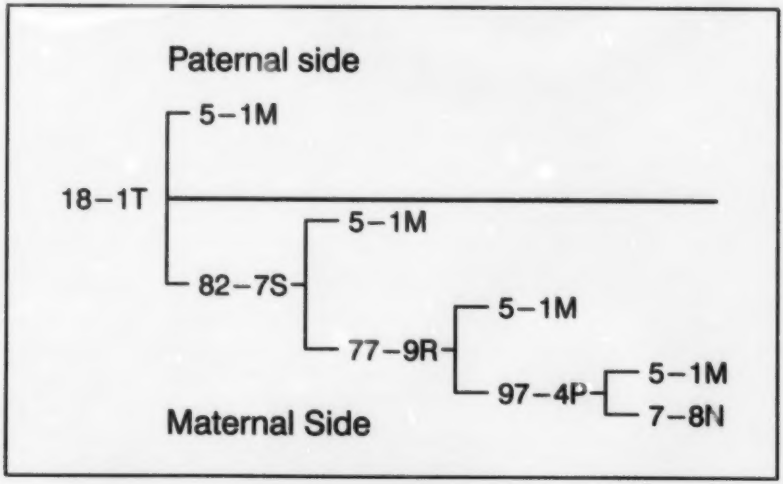
Paternal trace 14-2R and 3-1T are between 99-1P and Y, $n_p = 2$.
Maternal trace 29-9S and 11-1R are between Y and 99-1P, $n_m = 2$.

Table 12 Calculation of inbreeding for piglet Y

Common ancestor	n_p	n_m	+1	F_p	$(1 + F_{ca})$	F_a
29-9S	1	0	1	$(0.5)^2$	1 + 0.125	0.28125
99-1P	2	2	1	$(0.5)^5$	1 + 0	0.03125
					$F_y =$	0.3125
					or	31.25%

Example 3

A swine breeder produces a boar 18-1T by only using one sire. Given the following pedigree, how inbred is 18-1T?



In this pedigree, 5-1M is the common ancestor but he has three opportunities for his genes to get to 18-1T on the maternal side. Because there is no pedigree information available on 5-1M, we have to assume that he is not inbred. Based on this information, we proceed to step 4.

Step 4 Calculate the inbreeding of boar 18-1T (Table 13).

Paternal trace no animals between 5-1M and 18-1T, $n_p = 0$.
Maternal trace (1) 82-7S is between 18-1T and 5-1M, $n_m = 1$;
(2) 82-7S and 77-9R are between 18-1T and 5-1M, $n_m = 2$;
(3) 82-7S, 77-9R, and 97-4P are between 18-1T and 5-1M, $n_m = 3$.

Table 13 Calculation of inbreeding for boar 18-1T

Common ancestor	n_p	n_m	+1	F_p	$(1 + F_{ca})$	F_a
5-1M (1)	0	1	1	$(0.5)^2$	1 + 0	0.25
5-1M (2)	0	2	1	$(0.5)^3$	1 + 0	0.125
5-1M (3)	0	3	1	$(0.5)^4$	1 + 0	0.0625
					$F_{18\text{-}1T}$ =	0.4375
					or	43.75%

Practical management of inbreeding

Inbreeding cannot be ignored but calculating the inbreeding coefficients for all the animals in a herd is time-consuming. A short-cut is to scan the pedigrees of the potential parents to determine if they have common ancestors. To do this requires the producer to maintain detailed pedigrees on all breeding pigs in the herd. If there are no common ancestors, the litter will not be inbred. If there are common ancestors, the producer can calculate the inbreeding coefficient for the potential litter, and, based on how large it is, decide to either make the mating or not.

If the inbreeding coefficient is low (from 1 to 5%), the mating could be made with a low probability of negative effects. If the coefficient is greater than 5%, the mating probably should not be made. However, if all possible matings result in coefficients greater than 5%, then the producer needs to bring in some unrelated bloodlines. If inbreeding affects sow reproduction in any way then inbreeding levels must be reduced. Outcrossing inbred sows to unrelated boars reduces the inbreeding levels to zero in the offspring.

The size of the breeding herd, if closed to outside introductions, is an important consideration in managing inbreeding. It is a fact that the smaller the herd, the greater is the rate of inbreeding, as shown in Table 14.

Table 14 Rates of inbreeding as a percentage per generation for herds of various sizes

Number of gilts	Number of boars			
	5	10	15	20
	%			
5	5.00	–	–	–
10	3.75	2.50	–	–
15	3.33	2.08	1.67	–
20	3.13	1.88	1.46	1.25
25	3.00	1.75	1.33	1.13
30	2.92	1.67	1.25	1.04
35	2.86	1.61	1.19	0.98
40	2.81	1.56	1.15	0.94

Clearly, the rate of inbreeding decreases as the number of breeding boars or gilts, or both, increases. Thus, if it is economically feasible and if there is sufficient space and labor, expanding the size of the breeding herd can help to reduce the rate of inbreeding. The equation used to calculate the rate per generation is

$$\text{Rate} = (B + G)/(8 \times B \times G)$$

where: B is the number of breeding boars
G is the number of breeding females.

Where do we go from here?

The next 10 years have the potential for a number of changes in swine breeding in Canada. These changes include

- more use of AI
- more use of breeding stock from breeding companies
- methods of identifying pigs carrying genetic defects
- improvements to the national selection strategies for backfat thickness and growth rate
- effects of the Chinese pig on sow productivity
- effects of emerging technology in molecular genetics
- use of porcine somatotropin (PST) or beta-agonists to manipulate carcass composition.

With the emphasis being placed on herd health, expanding the use of AI is a logical step. Breeders, regardless of whether they are producing

purebred or crossbred animals, need to use the best animals available to genetically improve their herds. Promoting AI allows the widespread use of genetically superior boars with a minimum risk of introducing disease to the herd.

Related to this use is the increasing contribution of the breeding companies. Purchasing replacement gilts and boars from one rather than many herds lessens the chance of introducing disease to the herd. In addition, the breeding companies operate on a larger scale than do private breeders and can exert greater selection pressures on both production traits (backfat thickness and growth) and reproductive traits (such as litter size and nursing ability).

The following five changes could result from research that is under way:

1) The identification of carriers of genetic defects would result in a dramatic decrease in their incidence and corresponding economic losses. Scientists at the Agriculture Canada Research Station at Lacombe, Alta., have developed a method of identifying pigs that are carriers of the halothane gene.
2) National selection strategies for backfat thickness and growth rate could be altered as a result of the selection study under way at the Agriculture Canada Research Station at Brandon, Man. Upon its completion, the effects of prolonged selection for reduced backfat thickness and increased postweaning growth on reproductive performance and carcass quality will be known.
3) Chinese pigs, recently introduced into the United States, could dramatically change breeding strategies. Although these pigs as carcasses are inferior to Canadian pigs, their reproductive performance is outstanding. For example, gilts of the Meishan breed reach puberty by 100 days of age and wean larger litters (13–15 piglets). If genetics is the main determinant of these traits, incorporating genetic material from the Chinese breeds, by either gene transfer or crossbreeding, will improve the Canadian concept of sow productivity.
4) The emerging technology in molecular genetics will probably deal with genetic engineering and embryo manipulation. Such technologies when incorporated into commercial operations have to be maintained in the herds by using the principles described in this bulletin.
5) The use of porcine somatotropin and beta-agonists will alter not only carcass composition but also selection objectives. The effect of current selection practices for reducing fat composition and improving growth rate may affect the effectiveness of these factors. Another point that needs to be considered is how such pork is accepted by the consuming public.

Glossary of terms

(In the definitions, terms in boldface are defined in this list.)

AI Artificial insemination

allele Any of the possible forms of a **gene** at a specific location on a **chromosome**.

F_1 The first generation of progeny produced by mating animals from two different breeds.

backcross Mating F_1 animals to either parental breed.

chromosome The material that carries the **genes**.

crossbreeding The mating of animals from two different breeds.

dominant gene One of two **genes** at a specific location on a **chromosome** that masks the effect of the other **gene**.

estimated breeding value (EBV) An estimate of the genetic merit or value of an animal as a parent.

gene The basic unit of inheritance.

gene frequency The proportion of a **gene** that is present in a herd or population.

heritability The extent to which offspring performance results from **genes** transmitted from the parents.

heterosis or **hybrid vigor** The difference in performance between **crossbred** animals and the average performance of the parental breeds.

heterozygous The alleles at a specific location on a pair of **chromosomes** differ.

heterozygosity The tendency of the pairs of alleles at all locations on the **chromosomes** to differ.

homozygous The alleles at a specific location on a pair of **chromosomes** are the same.

homozygosity The tendency of the pairs of **alleles** at all locations on the chromosomes to be the same.

inbreeding The mating of related animals, which increases the chance that the **alleles** present at individual locations on each chromosome will be **homozygous**.

inbreeding coefficient The chance that each member of a pair of **alleles** present in an animal came from the same ancestor.

inbreeding depression The decrease in performance as inbreeding levels increase that is most evident in traits associated with fertility, survival, or rate of growth.

dependent culling levels A method of selecting for more than one trait in which the breeder sets standards for each trait and only those animals that meet or exceed all standards are chosen.

lethal genes **Genes** that cause the death of the animal when their effects are expressed.

malignant hyperthermia (MH) An uncontrollable increase in body temperature that may kill the animal.

migration The inflow of **genes** that results when breeding stock is introduced into a herd or the loss of **genes** that occurs when animals are culled.

mutation The process that changes a **gene** into an alternate form.

mutation rate The rate at which a **gene** is changed to an alternate form by a **mutation**.

nonlethal deleterious genes **Genes** that impair but do not directly kill the animal when their effects are expressed.

porcine stress syndrome (PSS) The sudden or unexpected death of pigs during transportation or normal daily activity.

qualitative trait A trait that is controlled by one or two pairs of **genes** and is not influenced by environmental or nongenetic effects to any great extent.

quantitative trait A trait that is controlled by many pairs of **genes** and is influenced by environmental or nongenetic effects.

random drift The changes in gene frequency that are due to chance.

recessive gene One of the two **alleles** at a specific location on a **chromosome** whose effect is masked by the other **allele**.

selection Allowing certain animals to produce more offspring than others.

selection differential The difference in performance between the selected animals and the average for all contemporary animals.

selection index A method of selecting for more than one trait in which the traits are combined into one score and animals are selected on the basis of this score.

standard deviation A measure of the variation associated with a specific trait.

tandem selection A method of selecting for more than one trait in which the breeder selects for one trait at a time.

CONVERSION FACTORS

Multiply an imperial number by the conversion factor given to get its metric equivalent.

Divide a metric number by the conversion factor given to get its equivalent in imperial units.

Imperial units	Approximate conversion factor	Metric units	
Length			
inch	25	millimetre	(mm)
foot	30	centimetre	(cm)
yard	0.9	metre	(m)
mile	1.6	kilometre	(km)
Area			
square inch	6.5	square centimetre	(cm^2)
square foot	0.09	square metre	(m^2)
square yard	0.836	square metre	(m^2)
square mile	259	hectare	(ha)
acre	0.40	hectare	(ha)
Volume			
cubic inch	16	cubic centimetre	(cm^3, mL, cc)
cubic foot	28	cubic decimetre	(dm^3)
cubic yard	0.8	cubic metre	(m^3)
fluid ounce	28	millilitre	(mL)
pint	0.57	litre	(L)
quart	1.1	litre	(L)
gallon (Imp.)	4.5	litre	(L)
gallon (U.S.)	3.8	litre	(L)
Weight			
ounce	28	gram	(g)
pound	0.45	kilogram	(kg)
short ton (2000 lb)	0.9	tonne	(t)

CALCULATING EXPONENTIALS

Multiplying 0.5 by an exponential power, say 2, is the same as

$$0.5 \times 0.5 = 0.25$$

To make the calculations easier, this table contains most values that would be needed to calculate inbreeding levels for most animals.

Exponential calculations for determining inbreeding coefficients

Calculation	Value
$(0.5)^1$	0.50
$(0.5)^2$	0.25
$(0.5)^3$	0.125
$(0.5)^4$	0.0625
$(0.5)^5$	0.03125
$(0.5)^6$	0.015625
$(0.5)^7$	0.0078125
$(0.5)^8$	0.00390625
$(0.5)^9$	0.001953125
$(0.5)^{10}$	0.0009765625
$(0.5)^{11}$	0.00048828125
$(0.5)^{12}$	0.000244140625